



1: AL050320. Human DNA sequenc...[gi:7263998]

LOCUS HSJ1077I2 107057 bp DNA linear PRI 25-OCT-2002
DEFINITION Human DNA sequence from clone RP5-1077I2 on chromosome 20 Contains the 3' end of the SPTLC2L gene for serine palmitoyltransferase long chain base subunit 2-like (aminotransferase 2), the 5' end of C20orf82 gene for a novel protein, part of 2 novel genes and a putative CpG island, complete sequence.
ACCESSION AL050320
VERSION AL050320.19 GI:7263998
KEYWORDS HTG; aminotransferase; CpG island; serine palmitoyltransferase; SPTLC2L.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 107057)
AUTHORS Smith, M.
TITLE Direct Submission
JOURNAL Submitted (22-OCT-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT On Mar 19, 2000 this sequence version replaced gi:6523711.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em.: EMBL; Sw.: SWISSPROT; Tr.: TREMBL; Wp.: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr20>
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP5-1077I2 is from the library RPCI-5 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>
VECTOR: pCYPAC2
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>

Contact: humquery@sanger.ac.uk

 IMPORTANT: This sequence is not the entire insert of clone RP5-1077I2. It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true right end of clone RP5-1077I2 is at 107057 in this sequence. The true right end of clone RP4-718P11 is at 100 in this sequence.

FEATURES	Location/Qualifiers
source	1..107057 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="20" /clone="RP5-1077I2" /clone_lib="RPCI-5"
<u>repeat region</u>	complement(64..135) /note="L3b repeat: matches 1389..1462 of consensus"
<u>repeat region</u>	complement(164..264) /note="MIR repeat: matches 54..149 of consensus"
<u>repeat region</u>	complement(274..490) /note="L1PA4 repeat: matches 5942..6155 of consensus"
<u>repeat region</u>	277..290 /note="4.7 copies 3 mer TTA 21% conserved"
gene	730..844 /gene="SPTLC2L"
<u>mRNA</u>	<730..844 /gene="SPTLC2L" /product="dJ1077I2.2 (serine palmitoyltransferase, long chain base subunit 2-like (aminotransferase 2), variant 1)" /note="continued from dJ718P11.1.1 in Em:AL109983 match: ESTs: Em:BQ011413" /evidence=not_experimental
<u>CDS</u>	<730..756 /gene="SPTLC2L" /note="continued from dJ718P11.1.1 in Em:AL109983" /codon_start=1 /evidence=not_experimental /product="dJ1077I2.2 (serine palmitoyltransferase, long chain base subunit 2-like (aminotransferase 2), variant 1)" /protein_id="CAD54807.1" /db_xref="GI:24412822" /db_xref="GOA:Q8IV87" /db_xref="SPTREMBL:Q8IV87" /translation="VICCVMKI"
<u>polyA signal</u>	824..829 /gene="SPTLC2L"
<u>polyA site</u>	844 /gene="SPTLC2L"
<u>repeat region</u>	884..896 /note="2.6 copies 5 mer AAAAT 26% conserved"
<u>repeat region</u>	992..1002 /note="2.2 copies 5 mer TTCTT 22% conserved"
<u>repeat region</u>	1473..1494 /note="11.0 copies 2 mer AC 44% conserved"
<u>repeat region</u>	1569..1580 /note="2.0 copies 6 mer CAAATG 24% conserved"
<u>repeat region</u>	1871..1883 /note="2.2 copies 6 mer TTTTCC 26% conserved"
<u>repeat region</u>	complement(2399..2464) /note="MER5A repeat: matches 41..105 of consensus"
<u>misc feature</u>	2513..2619 /note="match: STS: Em:Z94369"

repeat region 2665..2674
 /note="2.5 copies 4 mer GATG 20% conserved"
repeat region 3122..3136
 /note="3.8 copies 4 mer TCTT 21% conserved"
repeat region 3368..3378
 /note="2.2 copies 5 mer ACAA 22% conserved"
repeat region 3615..3649
 /note="2.7 copies 13 mer TTCATGATTTTAA 70% conserved"
repeat region 3833..3848
 /note="8.0 copies 2 mer CA 23% conserved"
repeat region 3889..3898
 /note="2.5 copies 4 mer TGGT 20% conserved"
repeat region 4108..4247
 /note="MER5A repeat: matches 44..184 of consensus"
repeat region 4367..4377
 /note="2.2 copies 5 mer CTTCT 22% conserved"
misc feature complement(4488..5147)
 /note="match: GSS: Em:AQ262066"
repeat region 4535..4556
 /note="5.5 copies 4 mer TCTT 35% conserved"
repeat region complement(4541..4855)
 /note="AluSp repeat: matches 1..313 of consensus"
repeat region 4554..4570
 /note="17.0 copies 1 mer T 34% conserved"
repeat region 4637..4648
 /note="2.0 copies 6 mer ACCTCC 24% conserved"
repeat region 5056..5066
 /note="3.7 copies 3 mer GAT 22% conserved"
repeat region 5325..5364
 /note="20.0 copies 2 mer TG 44% conserved"
repeat region 5450..5460
 /note="2.8 copies 4 mer AAAT 22% conserved"
repeat region complement(5498..5566)
 /note="LTR16A repeat: matches 382..444 of consensus"
repeat region complement(5567..5760)
 /note="MER63A repeat: matches 1..209 of consensus"
repeat region complement(5761..6016)
 /note="LTR16A repeat: matches 95..382 of consensus"
repeat region complement(6066..6288)
 /note="L1MC5 repeat: matches 7695..7923 of consensus"
misc feature 7638..8163
 /note="match: GSS: Em:B52469"
repeat region 8095..8512
 /note="HAL1 repeat: matches 827..1248 of consensus"
repeat region 8095..8108
 /note="2.3 copies 6 mer AATAGA 28% conserved"
repeat region 8328..8341
 /note="2.0 copies 7 mer TAAAAAT 28% conserved"
repeat region complement(8732..8854)
 /note="L1ME repeat: matches 5436..5565 of consensus"
repeat region 8803..8817
 /note="5.0 copies 3 mer TAT 21% conserved"
repeat region 8892..8902
 /note="5.5 copies 2 mer AT 22% conserved"
repeat region 8970..9267
 /note="HAL1 repeat: matches 1507..1818 of consensus"
repeat region complement(9338..9408)
 /note="MLT1J2 repeat: matches 252..323 of consensus"
repeat region 10186..10197
 /note="2.0 copies 6 mer TTTCAC 24% conserved"
repeat region 10789..11086
 /note="AluJb repeat: matches 1..297 of consensus"
repeat region 11073..11086
 /note="14.0 copies 1 mer A 28% conserved"
repeat region 11170..11523

<u>repeat region</u>	/note="THE1B repeat: matches 1..364 of consensus" 11576..11800
<u>repeat region</u>	/note="L1MED repeat: matches 2..249 of consensus" 11887..12242
<u>misc feature</u>	/note="L1MED repeat: matches 363..751 of consensus" complement(11947..12544)
<u>repeat region</u>	/note="match: STS: Em:AL110056" 12237..12248
<u>repeat region</u>	/note="2.0 copies 6 mer AGTAGA 24% conserved" 12365..12537
<u>repeat region</u>	/note="L1MED repeat: matches 904..1084 of consensus" complement(12529..13073)
<u>repeat region</u>	/note="L1MA5A repeat: matches 3652..4242 of consensus" 13076..13330
<u>repeat region</u>	/note="L1MA5A repeat: matches 4230..4483 of consensus" 13331..13638
<u>repeat region</u>	/note="AluSx repeat: matches 1..307 of consensus" 13614..13629
<u>repeat region</u>	/note="16.0 copies 1 mer A 23% conserved" 13639..15441
<u>repeat region</u>	/note="L1MA5A repeat: matches 4483..6294 of consensus" 14424..14447
<u>repeat region</u>	/note="8.0 copies 3 mer CAA 39% conserved" 14490..14500
<u>repeat region</u>	/note="2.8 copies 4 mer ACAT 22% conserved" 15063..15077
<u>repeat region</u>	/note="15.0 copies 1 mer A 30% conserved" 15091..15105
<u>repeat region</u>	/note="2.1 copies 7 mer AAGTAAA 30% conserved" 15169..15208
<u>repeat region</u>	/note="2.2 copies 18 mer GATACAAAATTACAGCTA 80% conserved" 15256..15266
<u>repeat region</u>	/note="3.7 copies 3 mer TAA 22% conserved" 15437..15453
<u>repeat region</u>	/note="2.8 copies 6 mer AAAAAT 25% conserved" 15775..15813
<u>repeat region</u>	/note="19.5 copies 2 mer TG 69% conserved" 16015..16037
<u>misc feature</u>	/note="1.9 copies 12 mer TGAGAGGCCTCT 37% conserved" complement(16370..16537)
<u>repeat region</u>	/note="match: GSS: Em:AQ044245" 16866..16878
<u>repeat region</u>	/note="2.6 copies 5 mer TTCCC 26% conserved" 17442..17817
<u>repeat region</u>	/note="LTR16C repeat: matches 85..489 of consensus" 17825..17836
<u>repeat region</u>	/note="2.4 copies 5 mer TCTTT 24% conserved" 18048..18267
<u>misc feature</u>	/note="MIR repeat: matches 12..247 of consensus" 18343..18706
<u>repeat region</u>	/note="match: GSS: Em:AQ099012" 18517..18616
<u>repeat region</u>	/note="L2 repeat: matches 2932..3031 of consensus" 18534..18544
<u>repeat region</u>	/note="3.7 copies 3 mer TTC 22% conserved" 18699..18714
<u>repeat region</u>	/note="3.2 copies 5 mer TGCAT 23% conserved" 19041..19141
<u>repeat region</u>	/note="L2 repeat: matches 3199..3312 of consensus" 19147..19156
<u>repeat region</u>	/note="2.5 copies 4 mer AAAT 20% conserved" 19309..19810
<u>repeat region</u>	/note="MLT1H repeat: matches 19..549 of consensus" 19673..19682
	/note="2.5 copies 4 mer CCAT 20% conserved"

<u>repeat region</u>	20051..20064
	/note="2.0 copies 7 mer AACAAATG 28% conserved"
<u>repeat region</u>	20123..20430
	/note="AluY repeat: matches 3..310 of consensus"
<u>repeat region</u>	20402..20418
	/note="17.0 copies 1 mer A 34% conserved"
<u>repeat region</u>	20416..20431
	/note="4.0 copies 4 mer AAAG 32% conserved"
<u>repeat region</u>	20437..20454
	/note="2.2 copies 8 mer TAGTGTGG 36% conserved"
<u>repeat region</u>	complement(20475..20589)
	/note="L2 repeat: matches 3197..3310 of consensus"
<u>repeat region</u>	20658..20667
	/note="3.3 copies 3 mer ATG 20% conserved"
<u>repeat region</u>	20704..20714
	/note="2.2 copies 5 mer ATTGT 22% conserved"
<u>repeat region</u>	20893..20904
	/note="2.0 copies 6 mer TCACAA 24% conserved"
<u>repeat region</u>	21003..21054
	/note="MLT1H repeat: matches 107..157 of consensus"
<u>repeat region</u>	21187..21290
	/note="MLT1F repeat: matches 414..503 of consensus"
<u>repeat region</u>	21404..21570
	/note="L1MC/D repeat: matches 5265..5449 of consensus"
<u>repeat region</u>	21450..21460
	/note="2.8 copies 4 mer AATA 22% conserved"
<u>repeat region</u>	22192..22765
	/note="L1MCc repeat: matches -514..418 of consensus"
<u>repeat region</u>	22348..22368
	/note="2.1 copies 10 mer GGGCATCCAG 42% conserved"
<u>repeat region</u>	22595..22606
	/note="2.0 copies 6 mer CTGGCT 24% conserved"
<u>repeat region</u>	22884..23840
	/note="L1MCc repeat: matches 435..1471 of consensus"
<u>repeat region</u>	23773..23786
	/note="4.7 copies 3 mer AAC 28% conserved"
<u>repeat region</u>	23789..23798
	/note="10.0 copies 1 mer A 20% conserved"
<u>repeat region</u>	23841..24130
	/note="AluSc repeat: matches 1..304 of consensus"
<u>repeat region</u>	24106..24130
	/note="25.0 copies 1 mer A 50% conserved"
<u>repeat region</u>	24131..24246
	/note="L1MCc repeat: matches 1471..1579 of consensus"
<u>repeat region</u>	24187..24198
	/note="2.0 copies 6 mer AAGGAT 24% conserved"
<u>repeat region</u>	24247..24456
	/note="MSTD repeat: matches 1..213 of consensus"
<u>repeat region</u>	24309..24327
	/note="9.5 copies 2 mer TA 29% conserved"
<u>repeat region</u>	24461..25134
	/note="L1MA5 repeat: matches 4023..4699 of consensus"
<u>repeat region</u>	24510..24519
	/note="3.3 copies 3 mer AAG 20% conserved"
<u>repeat region</u>	24696..24706
	/note="2.8 copies 4 mer AATA 22% conserved"
<u>repeat region</u>	25135..25562
	/note="MER57B repeat: matches 1..434 of consensus"
<u>repeat region</u>	25563..26664
	/note="L1PA17 repeat: matches 5026..6150 of consensus"
<u>repeat region</u>	25642..25656
	/note="2.5 copies 6 mer CAAAAG 21% conserved"
<u>repeat region</u>	25957..25967
	/note="2.2 copies 5 mer CAAAA 22% conserved"
<u>repeat region</u>	26656..26667

<u>repeat region</u>	/note="2.4 copies 5 mer AAAAG 24% conserved" 26665..28260
<u>repeat region</u>	/note="L1MA5 repeat: matches 4697..6294 of consensus" 27145..27155
<u>repeat region</u>	/note="2.8 copies 4 mer AACC 22% conserved" 27321..27335
<u>repeat region</u>	/note="15.0 copies 1 mer A 21% conserved" 27537..27547
<u>repeat region</u>	/note="2.2 copies 5 mer AAAAC 22% conserved" 27622..27634
<u>repeat region</u>	/note="2.6 copies 5 mer AAAGG 26% conserved" 27794..27809
<u>repeat region</u>	/note="2.0 copies 8 mer ATTTCTGC 25% conserved" 27920..27937
<u>repeat region</u>	/note="3.0 copies 6 mer TAGAAG 27% conserved" 27966..27978
<u>repeat region</u>	/note="2.6 copies 5 mer AGAGG 26% conserved" 28103..28112
<u>repeat region</u>	/note="2.5 copies 4 mer AAGA 20% conserved" 28280..28413
<u>repeat region</u>	/note="MSTD repeat: matches 249..388 of consensus" 28416..28624
<u>repeat region</u>	/note="L1MCc repeat: matches 1692..1885 of consensus" 28628..28911
<u>repeat region</u>	/note="AluJo repeat: matches 1..286 of consensus" 28911..28931
<u>repeat region</u>	/note="10.5 copies 2 mer AC 33% conserved" complement(28955..29226)
<u>repeat region</u>	/note="AluJo repeat: matches 1..252 of consensus" 29016..29026
<u>repeat region</u>	/note="2.2 copies 5 mer CTCAC 22% conserved" 29094..29116
<u>repeat region</u>	/note="23.0 copies 1 mer T 28% conserved" 29245..29262
<u>repeat region</u>	/note="2.0 copies 9 mer AAGTAACAA 36% conserved" 29273..29694
<u>repeat region</u>	/note="L1MCc repeat: matches 2043..2479 of consensus" 29535..29569
<u>repeat region</u>	/note="4.4 copies 8 mer AAAAAAGC 25% conserved" complement(29928..30344)
<u>repeat region</u>	/note="MLT1L repeat: matches 110..609 of consensus" 30011..30031
<u>repeat region</u>	/note="1.9 copies 11 mer AGAGAAAGGCC 33% conserved" complement(30285..30361)
<u>repeat region</u>	/note="LTR67 repeat: matches 97..174 of consensus" 30917..30967
<u>repeat region</u>	/note="25.5 copies 2 mer TG 93% conserved" 31093..31109
<u>repeat region</u>	/note="2.1 copies 8 mer AAAGAGAT 34% conserved" complement(31180..31295)
<u>repeat region</u>	/note="MLT1K repeat: matches 111..228 of consensus" 31292..31305
<u>repeat region</u>	/note="2.0 copies 7 mer TAAAATG 28% conserved" 31429..31438
<u>repeat region</u>	/note="3.3 copies 3 mer. TTC 20% conserved" 31509..31556
<u>repeat region</u>	/note="MADE1 repeat: matches 33..80 of consensus" 31669..32100
<u>repeat region</u>	/note="LTR16C repeat: matches 38..491 of consensus" 31776..31786
<u>repeat region</u>	/note="2.2 copies 5 mer AAGTC 22% conserved" 31901..31914
<u>repeat region</u>	/note="2.0 copies 7 mer TCACAGA 28% conserved" 32165..32175
<u>repeat region</u>	/note="2.2 copies 5 mer ATTTT 22% conserved"

repeat region 32453..32470
/note="3.6 copies 5 mer AAAGA 27% conserved"
repeat region 32571..32606
/note="2.1 copies 17 mer CAAGCTAGTAACTAAC 54% conserved"
repeat region 32790..32873
/note="L2 repeat: matches 2922..3014 of consensus"
repeat region 32897..32955
/note="Charlie5 repeat: matches 1..59 of consensus"
repeat region 33143..33152
/note="2.5 copies 4 mer ATAC 20% conserved"
repeat region 33916..33929
/note="2.0 copies 7 mer TTCCTC 28% conserved"
repeat region 34580..34591
/note="3.0 copies 4 mer ATAA 24% conserved"
repeat region complement(34609..34923)
/note="MLT1A repeat: matches 1..316 of consensus"
repeat region complement(34924..34993)
/note="L1MB1 repeat: matches 6082..6152 of consensus"
repeat region 34968..34978
/note="2.2 copies 5 mer ACAAT 22% conserved"
repeat region 34989..34999
/note="2.2 copies 5 mer AGGCA 22% conserved"
repeat region 35137..35170
/note="5.7 copies 6 mer TTTTTC 34% conserved"
repeat region 35150..35251
/note="25.5 copies 4 mer TTTC 150% conserved"
repeat region 35229..35286
/note="14.5 copies 4 mer TTCC 98% conserved"
repeat region complement(35285..35575)
/note="AluJo repeat: matches 1..294 of consensus"
repeat region 35447..35458
/note="12.0 copies 1 mer T 24% conserved"
repeat region 35588..35606
/note="3.8 copies 5 mer TTTTG 31% conserved"
repeat region 35654..35665
/note="2.0 copies 6 mer CTTATT 24% conserved"
repeat region 35729..35764
/note="2.4 copies 15 mer CCTTCCTTTCTCCCT 63% conserved"
repeat region 35767..35783
/note="4.2 copies 4 mer CCTC 25% conserved"
repeat region complement(35820..35892)
/note="L2 repeat: matches 3170..3243 of consensus"
repeat region 36014..36031
/note="3.0 copies 6 mer TATTTA 27% conserved"
repeat region 36866..36882
/note="8.5 copies 2 mer TC 34% conserved"
repeat region 37023..37077
/note="3.7 copies 15 mer AAAATGAAATAAAAC 67% conserved"
repeat region complement(37215..37423)
/note="MIR repeat: matches 31..261 of consensus"
repeat region 37273..37283
/note="2.8 copies 4 mer ATTA 22% conserved"
repeat region complement(37520..37798)
/note="L2 repeat: matches 2456..2742 of consensus"
repeat region 37766..37784
/note="3.8 copies 5 mer GGAGG 29% conserved"
repeat region 37896..37906
/note="2.8 copies 4 mer AAAG 22% conserved"
repeat region 37954..37965
/note="12.0 copies 1 mer A 24% conserved"
repeat region complement(38128..38424)
/note="AluSg repeat: matches 2..297 of consensus"
repeat region 38128..38144
/note="17.0 copies 1 mer T 34% conserved"
repeat region 38492..38911

<u>repeat region</u>	/note="MER63B repeat: matches 1..435 of consensus" 38494..38504
<u>repeat region</u>	/note="2.2 copies 5 mer GTGAT 22% conserved" complement(38945..39370)
<u>repeat region</u>	/note="MER57A repeat: matches 1..403 of consensus" 38967..38976
<u>repeat region</u>	/note="2.0 copies 5 mer AAATT 20% conserved" complement(39472..39532)
<u>repeat region</u>	/note="L2 repeat: matches 3205..3262 of consensus" complement(39534..39674)
<u>repeat region</u>	/note="MIR repeat: matches 108..259 of consensus" 39631..39640
<u>repeat region</u>	/note="3.3 copies 3 mer TAT 20% conserved" 39720..39729
<u>repeat region</u>	/note="2.5 copies 4 mer ATAA 20% conserved" 39931..39964
<u>repeat region</u>	/note="2.1 copies 16 mer ATGGATAAATAAATTA 59% conserved" 39935..39944
<u>repeat region</u>	/note="2.5 copies 4 mer ATAA 20% conserved" 39954..39967
<u>misc feature</u>	/note="3.5 copies 4 mer AATT 28% conserved" 40707..41300
<u>repeat region</u>	/note="match: GSS: Em:AG040344" 40893..40925
<u>repeat region</u>	/note="16.5 copies 2 mer TA 41% conserved" complement(40925..41068)
<u>repeat region</u>	/note="AluSg/x repeat: matches 145..288 of consensus" 41444..41755
<u>repeat region</u>	/note="L2 repeat: matches 2697..3050 of consensus" complement(41764..42122)
<u>repeat region</u>	/note="MLT1A repeat: matches 21..365 of consensus" 41860..41871
<u>repeat region</u>	/note="2.0 copies 6 mer TCAAGA 24% conserved" complement(42157..42433)
<u>repeat region</u>	/note="LTR16C repeat: matches 88..391 of consensus" 42162..42175
<u>repeat region</u>	/note="2.3 copies 6 mer AGTGAG 28% conserved" 42759..42771
<u>repeat region</u>	/note="2.2 copies 6 mer ATTTTA 26% conserved" complement(42785..42863)
<u>repeat region</u>	/note="MLT1J2 repeat: matches 368..448 of consensus" 42864..42880
<u>repeat region</u>	/note="2.1 copies 8 mer AAAATAAT 34% conserved" 42866..42885
<u>repeat region</u>	/note="6.7 copies 3 mer AAT 24% conserved" complement(42894..43239)
<u>repeat region</u>	/note="MLT1J2 repeat: matches 23..386 of consensus" 43074..43099
<u>repeat region</u>	/note="6.5 copies 4 mer AGAA 25% conserved" 43258..43274
<u>repeat region</u>	/note="2.4 copies 7 mer AAATTAG 25% conserved" complement(43270..43331)
<u>repeat region</u>	/note="MER113 repeat: matches 32..95 of consensus" 43285..43294
<u>misc feature</u>	/note="3.3 copies 3 mer TAA 20% conserved" 43413..43703
<u>repeat region</u>	/note="match: GSS: Em:AQ015991" complement(43476..43514)
<u>repeat region</u>	/note="MLT1H repeat: matches 538..577 of consensus" complement(43521..43739)
<u>repeat region</u>	/note="MLT1H repeat: matches 133..375 of consensus" 43708..43724
<u>repeat region</u>	/note="2.4 copies 7 mer CCACAAG 25% conserved" complement(43740..44231)
<u>repeat region</u>	/note="MLT2B2 repeat: matches 1..515 of consensus"

repeat region 43777..43811
/note="3.5 copies 10 mer AGACATAGAT 34% conserved"

repeat region 43787..43799
/note="3.2 copies 4 mer ATAG 26% conserved"

repeat region 43805..43829
/note="4.2 copies 6 mer ACAGAC 41% conserved"

repeat region 44002..44012
/note="2.8 copies 4 mer TCAA 22% conserved"

repeat region 44352..44361
/note="10.0 copies 1 mer A 20% conserved"

misc feature complement(44542..44977)
/note="match: GSS: Em:AQ358298"

repeat region 44830..45320
/note="MLT1H repeat: matches 1..549 of consensus"

repeat region 45523..45540
/note="2.2 copies 8 mer AAACATGA 27% conserved"

repeat region 45570..45674
/note="MLT1J2 repeat: matches 325..428 of consensus"

repeat region 45791..45806
/note="2.3 copies 7 mer ATTGATT 23% conserved"

misc feature 45853..46320
/note="match: GSS: Em:AQ186434"

repeat region complement(46233..46722)
/note="L1ME3 repeat: matches 5657..6158 of consensus"

repeat region 46777..46875
/note="L1ME3A repeat: matches 5743..5846 of consensus"

repeat region 46990..47021
/note="16.0 copies 2 mer GT 64% conserved"

repeat region 47140..47154
/note="5.0 copies 3 mer ATA 21% conserved"

repeat region 47427..47443
/note="2.4 copies 7 mer AGGAGAA 25% conserved"

repeat region 48160..48233
/note="MER58 repeat: matches 25..98 of consensus"

repeat region 48223..48253
/note="2.1 copies 15 mer TTTTAAATGGTCATA 44% conserved"

repeat region 48247..48348
/note="MER58 repeat: matches 2318..2417 of consensus"

repeat region 48457..48560
/note="MLT1J2 repeat: matches 32..133 of consensus"

repeat region 48655..48816
/note="MLT1J2 repeat: matches 288..450 of consensus"

repeat region 48880..48894
/note="7.5 copies 2 mer AC 30% conserved"

repeat region 50127..50602
/note="L1MC4 repeat: matches 7392..7858 of consensus"

repeat region 50173..50182
/note="2.0 copies 5 mer AACAT 20% conserved"

repeat region 50243..50255
/note="2.2 copies 6 mer ATACAA 26% conserved"

repeat region 50380..50393
/note="2.3 copies 6 mer ATGACA 28% conserved"

repeat region complement(50622..50888)
/note="MLT1H repeat: matches 224..531 of consensus"

repeat region 50893..50936
/note="22.0 copies 2 mer CA 88% conserved"

repeat region 50936..50998
/note="31.5 copies 2 mer AG 72% conserved"

repeat region complement(50977..51089)
/note="MLT1H repeat: matches 90..231 of consensus"

repeat region 51256..51413
/note="L1ME3A repeat: matches 5876..6065 of consensus"

repeat region 51508..51657
/note="MIR3 repeat: matches 23..179 of consensus"

repeat region complement(52443..52527)

<u>repeat region</u>	/note="L2 repeat: matches 3204..3312 of consensus" 52443..52452
<u>repeat region</u>	/note="2.5 copies 4 mer TTCA 20% conserved" complement(52602..52691)
<u>repeat region</u>	/note="MIR repeat: matches 101..187 of consensus" 52649..52666
<u>repeat region</u>	/note="2.0 copies 9 mer CAGACGAGG 27% conserved" 52772..52984
<u>repeat region</u>	/note="MER58A repeat: matches 1..223 of consensus" complement(53007..53400)
<u>repeat region</u>	/note="MLT1J2 repeat: matches 1..445 of consensus" 53222..53232
<u>repeat region</u>	/note="2.2 copies 5 mer AAAAG 22% conserved" 53515..53738
<u>repeat region</u>	/note="L1MC5 repeat: matches 7701..7928 of consensus" 53789..53812
<u>repeat region</u>	/note="4.8 copies 5 mer AAAAT 32% conserved" complement(54168..54323)
<u>repeat region</u>	/note="MLT1J2 repeat: matches 267..434 of consensus" 54341..54661
<u>repeat region</u>	/note="AluSx repeat: matches 1..312 of consensus" 54620..54632
<u>repeat region</u>	/note="13.0 copies 1 mer A 26% conserved" 54633..54647
<u>repeat region</u>	/note="3.8 copies 4 mer GAAT 30% conserved" 54646..54661
<u>repeat region</u>	/note="16.0 copies 1 mer A 23% conserved" 55244..55258
<u>repeat region</u>	/note="3.8 copies 4 mer ATTC 21% conserved" 55249..55270
<u>repeat region</u>	/note="1.8 copies 12 mer TTCATACATTTG 37% conserved" 55694..55705
<u>repeat region</u>	/note="2.0 copies 6 mer CCCTTT 24% conserved" 56046..56055
<u>repeat region</u>	/note="2.5 copies 4 mer AGTT 20% conserved" 56363..56373
<u>repeat region</u>	/note="2.8 copies 4 mer TTAT 22% conserved" 56397..58342
<u>misc feature</u>	/note="CpG island" /evidence=not_experimental
<u>repeat region</u>	56508..56526
<u>repeat region</u>	/note="3.8 copies 5 mer GGGCT 20% conserved" 57013..57027
<u>repeat region</u>	/note="3.0 copies 5 mer CTCCC 21% conserved" 57209..57220
<u>repeat region</u>	/note="2.0 copies 6 mer CTCCAG 24% conserved" 57255..57269
<u>repeat region</u>	/note="3.0 copies 5 mer CCACC 23% conserved" 57259..57271
<u>repeat region</u>	/note="3.2 copies 4 mer CCCA 26% conserved" 57458..57472
<u>repeat region</u>	/note="3.0 copies 5 mer GCGGC 21% conserved" 57534..57549
<u>repeat region</u>	/note="2.7 copies 6 mer GGCGAG 23% conserved" 57541..57654
<u>misc feature</u>	/note="Single clone region. single clone region containing only reads from a Short insert library of 20bae55h7. Assembly consistant with digest."
<u>repeat region</u>	57586..57659
<u>repeat region</u>	/note="24.7 copies 3 mer CCT 121% conserved" 57677..57689
<u>repeat region</u>	/note="2.2 copies 6 mer CCGCTC 26% conserved" 57699..58288
<u>repeat region</u>	/note="L1M2 repeat: matches 661..1268 of consensus" 57748..57769

<u>repeat region</u>	/note="4.4 copies 5 mer CCCGC 26% conserved" 57749..57762
<u>repeat region</u>	/note="4.7 copies 3 mer CCG 21% conserved" 57794..57807
<u>repeat region</u>	/note="2.8 copies 5 mer CCGGC 28% conserved" 57831..57843
<u>repeat region</u>	/note="2.2 copies 6 mer GTCTCC 26% conserved" 57841..57857
<u>repeat region</u>	/note="5.7 copies 3 mer CCG 34% conserved" 57926..57954
<u>repeat region</u>	/note="9.7 copies 3 mer GCG 49% conserved" 58021..58050
<u>repeat region</u>	/note="2.5 copies 12 mer GGAGCCCAGGCG 42% conserved" 58057..58073
<u>repeat region</u>	/note="2.1 copies 8 mer CCGGGCTC 34% conserved" 58070..58085
<u>repeat region</u>	/note="5.3 copies 3 mer CTC 23% conserved" 58096..58122
<u>repeat region</u>	/note="9.0 copies 3 mer CCG 38% conserved" 58098..58122
<u>repeat region</u>	/note="3.6 copies 7 mer GCCGCCG 34% conserved" 58170..58199
<u>repeat region</u>	/note="10.0 copies 3 mer GCT 42% conserved" 58238..58257
<u>repeat region</u>	/note="2.0 copies 10 mer CCGACGCGGC 33% conserved" 58518..58527
<u>repeat region</u>	/note="2.5 copies 4 mer TCTG 20% conserved" 58603..58612
<u>repeat region</u>	/note="2.5 copies 4 mer TGCT 20% conserved" 58836..58847
<u>repeat region</u>	/note="2.0 copies 6 mer TTCCTC 24% conserved" 59256..59559
<u>repeat region</u>	/note="AluSx repeat: matches 3..312 of consensus" 59530..59564
<u>repeat region</u>	/note="35.0 copies 1 mer A 25% conserved" 59531..59593
<u>repeat region</u>	/note="12.6 copies 5 mer AAAAT 80% conserved" 59646..59664
<u>repeat region</u>	/note="1.9 copies 10 mer CTTTATACAT 29% conserved" complement(59700..59873)
<u>misc feature</u>	/note="MIR repeat: matches 82..260 of consensus" 60390..60614
	/note="match: GSS: Em:AQ046228 match: STS: Em:G50471"
<u>repeat region</u>	60507..60518
<u>repeat region</u>	/note="2.0 copies 6 mer CAGCTT 24% conserved" 60828..60837
<u>repeat region</u>	/note="2.5 copies 4 mer TTCT 20% conserved" 61115..61124
<u>repeat region</u>	/note="3.3 copies 3 mer AGT 20% conserved" complement(61136..61206)
<u>repeat region</u>	/note="MIR repeat: matches 193..262 of consensus" 61206..61217
<u>repeat region</u>	/note="3.0 copies 4 mer CTTT 24% conserved" complement(61207..61525)
<u>repeat region</u>	/note="AluY repeat: matches 1..311 of consensus" 61215..61236
<u>repeat region</u>	/note="22.0 copies 1 mer T 44% conserved" 61386..61399
<u>repeat region</u>	/note="14.0 copies 1 mer T 28% conserved" complement(61526..61637)
<u>repeat region</u>	/note="MIR repeat: matches 77..193 of consensus" 61798..61812
<u>repeat region</u>	/note="7.5 copies 2 mer AT 21% conserved" 62222..62233

repeat region /note="2.0 copies 6 mer TTAATG 24% conserved"
62245..62271

repeat region /note="4.5 copies 6 mer ATAGAT 45% conserved"
62788..62798

repeat region /note="11.0 copies 1 mer T 22% conserved"
complement(62812..63323)

repeat region /note="MLT1H repeat: matches 18..549 of consensus"
complement(63386..63567)

repeat region /note="L1M4 repeat: matches 2247..2434 of consensus"
complement(63587..63875)

repeat region /note="AluY repeat: matches 1..289 of consensus"
63591..64190

repeat region /note="15.0 copies 40 mer
TTTTGAGACGGAGTCTCACTCTATCACCCAGGCTGGAGTG 909% conserved"
complement(63880..64180)

repeat region /note="AluY repeat: matches 1..301 of consensus"
63880..63899

repeat region /note="20.0 copies 1 mer T 31% conserved"
64188..64197

repeat region /note="2.0 copies 5 mer TTAA 20% conserved"
64321..64331

repeat region /note="3.7 copies 3 mer GCT 22% conserved"
complement(64333..64645)

repeat region /note="AluSx repeat: matches 1..305 of consensus"
64333..64355

repeat region /note="23.0 copies 1 mer T 37% conserved"
64645..64658

repeat region /note="4.7 copies 3 mer CTG 28% conserved"
complement(64676..65154)

repeat region /note="HAL1 repeat: matches 1214..1726 of consensus"
64852..64861

repeat region /note="2.0 copies 5 mer AATTT 20% conserved"
65434..65470

repeat region /note="3.4 copies 11 mer CTTTTCTTTC 51% conserved"
65446..65528

repeat region /note="20.8 copies 4 mer CTTT 37% conserved"
65475..65487

repeat region /note="2.6 copies 5 mer TTCCT 26% conserved"
65505..65524

repeat region /note="10.0 copies 2 mer TC 33% conserved"
65532..65550

repeat region /note="1.9 copies 10 mer TTTTTTAAAG 38% conserved"
complement(65542..66060)

repeat region /note="L1ME2 repeat: matches 5634..6164 of consensus"
66207..66216

repeat region /note="5.0 copies 2 mer CT 20% conserved"
complement(66506..66872)

repeat region /note="L3b repeat: matches 1114..1476 of consensus"
66655..66673

repeat region /note="2.1 copies 9 mer TGTTCACTT 38% conserved"
66945..66955

repeat region /note="2.2 copies 5 mer AAAGA 22% conserved"
67043..67053

repeat region /note="2.2 copies 5 mer GATGG 22% conserved"
67091..67100

repeat region /note="2.5 copies 4 mer CAAA 20% conserved"
67118..67147

repeat region /note="6.0 copies 5 mer AGAAA 44% conserved"
67120..67148

repeat region /note="29.0 copies 1 mer A 31% conserved"
67189..67206

repeat region /note="2.0 copies 9 mer TTATAAGAA 36% conserved"
67235..67247

repeat region /note="3.2 copies 4 mer TTTC 26% conserved"
67311..67498

<u>repeat region</u>	/note="LTR16C repeat: matches 289..488 of consensus" 67609..67618
<u>repeat region</u>	/note="3.3 copies 3 mer TTG 20% conserved" 68515..68525
<u>repeat region</u>	/note="3.7 copies 3 mer TTA 22% conserved" complement(68524..68539)
<u>repeat region</u>	/note="L1MA10 repeat: matches 6319..6334 of consensus" complement(68540..69072)
<u>repeat region</u>	/note="L1ME1 repeat: matches 5582..6161 of consensus" 68776..68790
<u>repeat region</u>	/note="3.0 copies 5 mer TGCAT 21% conserved" 68816..68825
<u>repeat region</u>	/note="2.5 copies 4 mer ATTC 20% conserved" 69398..69414
<u>repeat region</u>	/note="17.0 copies 1 mer A 25% conserved" 69473..69489
<u>repeat region</u>	/note="1.9 copies 9 mer ATTCTCTTG 27% conserved" 69481..69508
<u>repeat region</u>	/note="2.2 copies 13 mer ATTCTCTTGCCCC 40% conserved" 69688..69987
<u>repeat region</u>	/note="AluSp repeat: matches 2..302 of consensus" 69969..69987
<u>repeat region</u>	/note="19.0 copies 1 mer A 38% conserved" 70233..70333
<u>repeat region</u>	/note="MER5A repeat: matches 9..112 of consensus" complement(70347..71285)
<u>repeat region</u>	/note="L1PB4 repeat: matches 5215..6152 of consensus" 70594..70605
<u>repeat region</u>	/note="2.0 copies 6 mer TTTCTG 24% conserved" 71051..71065
<u>repeat region</u>	/note="2.5 copies 6 mer TTTTAA 21% conserved" 71104..71128
<u>repeat region</u>	/note="2.3 copies 11 mer TTGTTGTCCTC 32% conserved" 71286..71350
<u>repeat region</u>	/note="MER5A repeat: matches 124..189 of consensus" 71430..71439
<u>repeat region</u>	/note="3.3 copies 3 mer TAA 20% conserved" 71501..71516
<u>repeat region</u>	/note="2.0 copies 8 mer CATGGGTC 32% conserved" complement(71650..71724)
<u>repeat region</u>	/note="MLT1I repeat: matches 104..180 of consensus" 71726..71873
<u>repeat region</u>	/note="MIR repeat: matches 25..183 of consensus" 72208..72223
<u>repeat region</u>	/note="4.0 copies 4 mer TTCC 23% conserved" complement(72301..72592)
<u>repeat region</u>	/note="AluSc repeat: matches 4..294 of consensus" 72301..72315
<u>repeat region</u>	/note="15.0 copies 1 mer T 21% conserved" 72378..72389
<u>repeat region</u>	/note="2.0 copies 6 mer ACCTCC 24% conserved" 72445..72454
<u>repeat region</u>	/note="3.3 copies 3 mer CCA 20% conserved" complement(72715..72839)
<u>repeat region</u>	/note="THE1A repeat: matches 1..126 of consensus" complement(72840..73499)
<u>repeat region</u>	/note="THE1A-int repeat: matches 918..1580 of consensus" 72941..72960
<u>repeat region</u>	/note="2.9 copies 7 mer AAAGTCC 31% conserved" 73481..73492
<u>repeat region</u>	/note="2.0 copies 6 mer CCCTGC 24% conserved" complement(73505..73581)
<u>repeat region</u>	/note="THE1A repeat: matches 1..80 of consensus" 73583..74087
<u>repeat region</u>	/note="L1ME3A repeat: matches 5610..6157 of consensus"

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gene complement(join(74174..74482,75357..75477,75826..76047))
      /gene="dJ1077I2.4"
mRNA complement(join(74174..74482,75357..75477,75826..76047))
      /gene="dJ1077I2.4"
      /product="dJ1077I2.4 (Putative novel transcript)"
      /note="match: ESTs: Em:BI463885"
      /evidence=not_experimental
repeat region 74749..74764
      /note="2.0 copies 8 mer GGCAAAAT 32% conserved"
repeat region 75388..75401
      /note="2.0 copies 7 mer AGTGTGA 28% conserved"
repeat region 75754..75766
      /note="2.2 copies 6 mer TGGCCT 26% conserved"
repeat region 75818..75827
      /note="2.5 copies 4 mer TTAC 20% conserved"
repeat region 76136..76145
      /note="2.0 copies 5 mer TCATT 20% conserved"
repeat region 76515..76528
      /note="3.5 copies 4 mer CATT 28% conserved"
repeat region complement(76516..77245)
      /note="L2 repeat: matches 2448..3313 of consensus"
repeat region 77144..77153
      /note="2.5 copies 4 mer TGGA 20% conserved"
repeat region complement(77281..77325)
      /note="L2 repeat: matches 2304..2348 of consensus"
repeat region complement(77352..78690)
      /note="L2 repeat: matches 586..2082 of consensus"
repeat region 78727..78736
      /note="2.5 copies 4 mer TTTG 20% conserved"
repeat region 78739..78756
      /note="3.0 copies 6 mer GTTTTT 27% conserved"
repeat region complement(79263..79475)
      /note="MIR repeat: matches 10..241 of consensus"
repeat region 79532..79626
      /note="MIR repeat: matches 34..130 of consensus"
repeat region complement(79628..79686)
      /note="MLT1J1 repeat: matches 265..326 of consensus"
repeat region complement(79699..79732)
      /note="MLT1I repeat: matches 127..160 of consensus"
gene complement(join(80437..80754,81615..81742))
      /gene="dJ1077I2.3"
mRNA complement(join(80437..80754,81615..81742))
      /gene="dJ1077I2.3"
      /product="dJ1077I2.3 (Putative novel transcript)"
      /note="match: ESTs: Em:BF510052"
      /evidence=not_experimental
polyA site complement(80439)
      /gene="dJ1077I2.3"
repeat region 80508..80518
      /note="2.8 copies 4 mer ACAG 22% conserved"
repeat region 80761..80774
      /note="14.0 copies 1 mer A 28% conserved"
repeat region 81478..81489
      /note="3.0 copies 4 mer CTTC 24% conserved"
repeat region complement(81491..81658)
      /note="MLT1E repeat: matches 439..593 of consensus"
repeat region complement(81652..81945)
      /note="MLT1E repeat: matches 1..303 of consensus"
repeat region 82056..82073
      /note="3.6 copies 5 mer TTCAT 27% conserved"
repeat region 82067..82082
      /note="2.3 copies 7 mer TCATTTC 32% conserved"
repeat region 82072..82089
      /note="2.0 copies 9 mer TCTCATTTC 27% conserved"
repeat region 82359..82660

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<u>repeat region</u>	/note="AluSx repeat: matches 1..297 of consensus" 82646..82660
<u>repeat region</u>	/note="15.0 copies 1 mer A 30% conserved" complement(82983..83071)
<u>repeat region</u>	/note="MIR repeat: matches 47..144 of consensus" 83149..83158
<u>repeat region</u>	/note="2.0 copies 5 mer CTTTT 20% conserved" 83257..83266
<u>repeat region</u>	/note="10.0 copies 1 mer T 20% conserved" 83311..83325
<u>repeat region</u>	/note="7.5 copies 2 mer AT 21% conserved" 83328..83621
<u>repeat region</u>	/note="AluSq repeat: matches 2..299 of consensus" 83606..83615
<u>repeat region</u>	/note="10.0 copies 1 mer A 20% conserved" 83891..83932
<u>repeat region</u>	/note="21.0 copies 2 mer GT 84% conserved" 83931..83943
<u>repeat region</u>	/note="3.2 copies 4 mer GTAG 26% conserved" 84233..84247
<u>repeat region</u>	/note="7.5 copies 2 mer GT 21% conserved" 84562..84573
<u>repeat region</u>	/note="2.0 copies 6 mer TATTCT 24% conserved" 85418..85429
<u>repeat region</u>	/note="2.4 copies 5 mer GGTCA 24% conserved" 85511..85521
<u>repeat region</u>	/note="2.2 copies 5 mer AAATA 22% conserved" 86153..86211
<u>repeat region</u>	/note="11.8 copies 5 mer GTTTT 118% conserved" 86312..86322
<u>repeat region</u>	/note="2.2 copies 5 mer TAATG 22% conserved" complement(86895..87015)
<u>repeat region</u>	/note="MER5B repeat: matches 54..172 of consensus" 87029..87150
<u>repeat region</u>	/note="L2 repeat: matches 3144..3272 of consensus" 87464..87474
<u>repeat region</u>	/note="2.8 copies 4 mer CCTC 22% conserved" 87614..87624
<u>repeat region</u>	/note="2.2 copies 5 mer TTCCA 22% conserved" 87870..88316
<u>misc feature</u>	/note="match: GSS: Em:AQ457776"
<u>repeat region</u>	88004..88016
<u>repeat region</u>	/note="2.2 copies 6 mer AGCTAG 26% conserved" 88039..88048
<u>repeat region</u>	/note="2.5 copies 4 mer AGCA 20% conserved" 88332..88345
<u>repeat region</u>	/note="3.5 copies 4 mer AAGC 28% conserved" 88590..88599
<u>repeat region</u>	/note="2.5 copies 4 mer TGAA 20% conserved" 88730..88741
<u>repeat region</u>	/note="2.0 copies 6 mer AAAAGT 24% conserved" 88842..89139
<u>repeat region</u>	/note="AluSx repeat: matches 1..293 of consensus" 88962..88978
<u>repeat region</u>	/note="2.1 copies 8 mer AAAAATAC 34% conserved" 89129..89139
<u>repeat region</u>	/note="11.0 copies 1 mer A 22% conserved" complement(89924..90101)
<u>repeat region</u>	/note="MER5A repeat: matches 6..189 of consensus" 90107..90117
<u>repeat region</u>	/note="2.2 copies 5 mer AATTA 22% conserved" 90203..90214
<u>repeat region</u>	/note="2.0 copies 6 mer TAAAAT 24% conserved" 90216..90227
<u>repeat region</u>	/note="2.0 copies 6 mer ACACAT 24% conserved"

<u>repeat region</u>	90226..90239 /note="2.3 copies 6 mer ATCCAT 28% conserved"
<u>repeat region</u>	90236..90251 /note="8.0 copies 2 mer AT 32% conserved"
<u>repeat region</u>	90251..90261 /note="5.5 copies 2 mer TG 22% conserved"
<u>repeat region</u>	90309..90630 /note="AluSx repeat: matches 1..307 of consensus"
<u>repeat region</u>	90432..90452 /note="21.0 copies 1 mer A 42% conserved"
<u>repeat region</u>	90608..90630 /note="5.8 copies 4 mer AAAT 46% conserved"
<u>repeat region</u>	90655..90675 /note="10.5 copies 2 mer AT 24% conserved"
<u>repeat region</u>	90658..90674 /note="2.8 copies 6 mer TATATT 34% conserved"
<u>repeat region</u>	90678..90690 /note="2.2 copies 6 mer CATATA 26% conserved"
<u>repeat region</u>	90794..90806 /note="2.2 copies 6 mer TCAGAA 26% conserved"
<u>repeat region</u>	91258..91267 /note="2.5 copies 4 mer TTCC 20% conserved"
<u>repeat region</u>	complement(91289..91616) /note="L2 repeat: matches 2982..3312 of consensus"
<u>repeat region</u>	91291..91300 /note="2.5 copies 4 mer CATT 20% conserved"
<u>repeat region</u>	91549..91558 /note="5.0 copies 2 mer CT 20% conserved"
<u>repeat region</u>	91758..91768 /note="5.5 copies 2 mer TG 22% conserved"
<u>repeat region</u>	91819..91830 /note="2.4 copies 5 mer AAAAG 24% conserved"
<u>repeat region</u>	complement(91840..91994) /note="L2 repeat: matches 2945..3108 of consensus"
<u>repeat region</u>	complement(92094..92166) /note="MER91A repeat: matches 8..82 of consensus"
<u>repeat region</u>	92259..92272 /note="3.5 copies 4 mer CATT 28% conserved"
<u>repeat region</u>	92299..92309 /note="11.0 copies 1 mer T 22% conserved"
<u>repeat region</u>	92487..92791 /note="AluSx repeat: matches 1..305 of consensus"
<u>repeat region</u>	92695..92706 /note="2.0 copies 6 mer GGAGGT 24% conserved"
<u>repeat region</u>	92769..92791 /note="23.0 copies 1 mer A 46% conserved"
<u>repeat region</u>	92910..92927 /note="2.2 copies 8 mer GGGATCAT 36% conserved"
<u>repeat region</u>	93142..93196 /note="MIR repeat: matches 113..163 of consensus"
<u>repeat region</u>	93281..93298 /note="2.0 copies 9 mer AGGTGGAGG 36% conserved"
<u>repeat region</u>	93288..93300 /note="2.2 copies 6 mer GGAGGT 26% conserved"
<u>repeat region</u>	93398..93408 /note="2.2 copies 5 mer AGAGA 22% conserved"
<u>repeat region</u>	complement(93452..93501) /note="MIR repeat: matches 91..144 of consensus"
<u>repeat region</u>	93557..93568 /note="2.4 copies 5 mer AAAAT 24% conserved"
<u>repeat region</u>	93566..93577 /note="2.0 copies 6 mer TAACAG 24% conserved"
<u>repeat region</u>	93606..93832 /note="AluSq repeat: matches 1..225 of consensus"
<u>repeat region</u>	93751..93760

<u>repeat region</u>	/note="3.3 copies 3 mer GTG 20% conserved" 94085..94098
<u>repeat region</u>	/note="14.0 copies 1 mer A 28% conserved" 94355..94452
<u>repeat region</u>	/note="MIR repeat: matches 111..219 of consensus" 94503..94647
<u>repeat region</u>	/note="LTR33 repeat: matches 14..160 of consensus" 94674..94898
<u>repeat region</u>	/note="LTR33 repeat: matches 301..521 of consensus" 95374..95677
<u>repeat region</u>	/note="AluSx repeat: matches 1..306 of consensus" 95654..95677
<u>repeat region</u>	/note="24.0 copies 1 mer A 30% conserved" complement(95813..96278)
<u>repeat region</u>	/note="LTR37B repeat: matches 1..468 of consensus" 95893..95902
<u>repeat region</u>	/note="2.5 copies 4 mer AATG 20% conserved" 95972..95981
<u>repeat region</u>	/note="3.3 copies 3 mer ATG 20% conserved" 96295..96360
<u>repeat region</u>	/note="L2 repeat: matches 3198..3268 of consensus" 96404..96415
<u>repeat region</u>	/note="2.4 copies 5 mer AGCTA 24% conserved" 96976..96989
<u>repeat region</u>	/note="14.0 copies 1 mer T 28% conserved" complement(97136..97231)
<u>repeat region</u>	/note="MLT1H repeat: matches 453..549 of consensus" complement(97339..97441)
<u>repeat region</u>	/note="MLT1H repeat: matches 197..305 of consensus" 97505..97822
<u>misc feature</u>	/note="AluSq repeat: matches 1..307 of consensus" 97582..98164
<u>repeat region</u>	/note="match: GSS: Em:AQ318861" 97649..97661
<u>repeat region</u>	/note="4.3 copies 3 mer GTG 26% conserved" 97799..97819
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<u>repeat region</u>	/note="MIR repeat: matches 17..113 of consensus" 97968..97983
<u>repeat region</u>	/note="2.7 copies 6 mer GACCCA 32% conserved" 98280..98295
<u>repeat region</u>	/note="2.7 copies 6 mer GCCTGG 23% conserved" 98622..98640
<u>repeat region</u>	/note="1.9 copies 10 mer CTGGTGGCCA 38% conserved" 98636..98646
<u>repeat region</u>	/note="2.2 copies 5 mer TGGCC 22% conserved" 98827..98849
<u>misc feature</u>	/note="23.0 copies 1 mer T 28% conserved" complement(98879..99267)
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<u>repeat region</u>	/note="2.5 copies 4 mer TCCA 20% conserved" 100252..100265
<u>repeat region</u>	/note="2.0 copies 7 mer TGTGTGT 28% conserved" 100409..100419
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<u>repeat region</u>	/note="3.0 copies 9 mer ACTCTGACC 36% conserved" 101677..101688
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